

=====

Sequence Listing could not be accepted due to errors.

See attached Validation Report.

If you need help call the Patent Electronic Business Center at (866) 217-9197 (toll free).

Reviewer: Keisha Douglas

Timestamp: [year=2008; month=8; day=18; hr=16; min=40; sec=32; ms=968;]

=====

Reviewer Comments:

<210> 3

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<221> VARIANT

<222> (3,4,5,9,10,11)

<223> encoded by randomized DNA sequence: Ala, Cys, Asp, Glu, Phe, Gly, His, Ile, Lys, Leu, Met, Asn, Pro, Gln, Arg, Ser, Thr, Val, Trp, Tyr

<400> 3

Please explain <213> 'Artificial' in the above sequence id# 3. Please also correct the remaining sequences showing similar errors.

Application No: 10581431 Version No: 1.0

Input Set:

Output Set:

Started: 2008-07-17 10:31:50.877
Finished: 2008-07-17 10:31:52.817
Elapsed: 0 hr(s) 0 min(s) 1 sec(s) 940 ms
Total Warnings: 31
Total Errors: 3
No. of SeqIDs Defined: 72
Actual SeqID Count: 72

Error code	Error Description
W 213	Artificial or Unknown found in <213> in SEQ ID (1)
W 213	Artificial or Unknown found in <213> in SEQ ID (2)
W 213	Artificial or Unknown found in <213> in SEQ ID (3)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (3)
W 213	Artificial or Unknown found in <213> in SEQ ID (4)
W 213	Artificial or Unknown found in <213> in SEQ ID (5)
W 213	Artificial or Unknown found in <213> in SEQ ID (6)
W 213	Artificial or Unknown found in <213> in SEQ ID (7)
W 213	Artificial or Unknown found in <213> in SEQ ID (8)
W 213	Artificial or Unknown found in <213> in SEQ ID (9)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (9)
W 213	Artificial or Unknown found in <213> in SEQ ID (10)
W 213	Artificial or Unknown found in <213> in SEQ ID (11)
W 213	Artificial or Unknown found in <213> in SEQ ID (12)
W 213	Artificial or Unknown found in <213> in SEQ ID (13)
W 213	Artificial or Unknown found in <213> in SEQ ID (14)
W 213	Artificial or Unknown found in <213> in SEQ ID (15)
W 213	Artificial or Unknown found in <213> in SEQ ID (16)
W 213	Artificial or Unknown found in <213> in SEQ ID (17)

Input Set:

Output Set:

Started: 2008-07-17 10:31:50.877
Finished: 2008-07-17 10:31:52.817
Elapsed: 0 hr(s) 0 min(s) 1 sec(s) 940 ms
Total Warnings: 31
Total Errors: 3
No. of SeqIDs Defined: 72
Actual SeqID Count: 72

Error code	Error Description
W 213	Artificial or Unknown found in <213> in SEQ ID (18)
W 213	Artificial or Unknown found in <213> in SEQ ID (20)
W 213	Artificial or Unknown found in <213> in SEQ ID (21) This error has occurred more than 20 times, will not be displayed
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (22)

<110> The Scripps Research Institute

<120> INTEGRIN ALPHA.IIb.BETA.3 SPECIFIC ANTIBODIES AND PEPTIDES

<130> TSRI 1019.1 US

<140> 10581431

<141> 2008-07-17

<150> US 60/526,859

<151> 2003-12-03

<150> PCT/US2004/040381

<151> 2004-12-03

<160> 72

<210> 1

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> HCDR3 part

<400> 1

Cys Ser Phe Gly Arg Gly Asp Ile Arg Asn Cys

1

5

10

<210> 2

<211> 11

<212> PRT

<213> Artificial Sequence

<220>

<223> HCDR3 part

<400> 2

Gly Ser Phe Gly Arg Gly Asp Ile Arg Asn Gly

1

5

10

<210> 3

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<221> VARIANT

<222> (3, 4, 5, 9, 10, 11)

<223> encoded by randomized DNA sequence: Ala, Cys, Asp, Glu, Phe, Gly, His, Ile, Lys, Leu, Met, Asn, Pro, Gln, Arg, Ser, Thr, Val, Trp, Tyr

<400> 3

Val Gly Xaa Xaa Xaa Arg Ala Asp Xaa Xaa Xaa Tyr Ala Met Asp
1 5 10 15
Val

<210> 4

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> HCDR3 consensus part

<400> 4

Val Val Cys Arg Ala Asp Lys Arg Cys
1 5

<210> 5

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> HCDR3 consensus part

<400> 5

Val Trp Cys Arg Ala Asp Arg Arg Cys
1 5

<210> 6

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> HCDR3 consensus part

<400> 6

Val Trp Cys Arg Ala Asp Lys Arg Cys
1 5

<210> 7

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> HCDR3 consensus part

<400> 7

Val Val Cys Arg Ala Asp Arg Arg Cys
1 5

<210> 8

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> CDR consensus part

<400> 8

Val Arg Val Val Cys Arg Ala Asp Arg Arg Cys Tyr Ala Met Asp
1 5 10 15

Val

<210> 9

<211> 72

<212> DNA

<213> Artificial Sequence

<220>

<221> misc_feature

<222> (25,26,28,29,31,32,43,44,46,47,49,50)

<223> primer neo-rad-f; encoded by randomized DNA sequence: a, g, c, t

<220>

<221> misc_feature

<222> (27,30,33,45,48,51)

<223> primer neo-rad-f; encoded by randomized DNA sequence: g, t

<400> 9

gtgttattact gtgcgagagt ggggnnknnk nnkcggtgccg acnnknnknn ktacgctatg 60

gacgtctggg gc 72

<210> 10

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> primer dpseq

<400> 10

agaagcgtag tccggAACGT C 21

<210> 11

<211> 57
<212> DNA
<213> Artificial Sequence

<220>
<223> primer DP-47N-term

<400> 11

gctgccccaac cagccatggc cgaggtgcag ctgttggagt ctgggggagg cttggta 57

<210> 12
<211> 39
<212> DNA
<213> Artificial Sequence

<220>
<223> primer DP-47FR3

<400> 12

cactctcgca cagtaataca cggccgtgtc ctggctct 39

<210> 13
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> primer lead-VH

<400> 13

ggccatggct ggttgggcag c 21

<210> 14
<211> 39
<212> DNA
<213> Artificial Sequence

<220>
<223> primer dp-EX

<400> 14

gaggaggagg aggaggagag aagcgtagtc cggaacgtc 39

<210> 15
<211> 24
<212> DNA
<213> Artificial Sequence
<220>
<223> primer ompseq

<400> 15

aagacagcta tcgcgattgc agtg

24

<210> 16

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> primer leadB

<400> 16

ggccatggct ggttgggcag c

21

<210> 17

<211> 41

<212> DNA

<213> Artificial Sequence

<220>

<223> primer RSC-F

<400> 17

gaggaggagg aggaggaggc ggggcccagg cggccgagct c

41

<210> 18

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> primer lead-B

<400> 18

ggccatggct ggttgggcag c

21

<210> 19

<211> 9

<212> PRT

<213> Homo sapiens

<400> 19

Thr His Ser Arg Ala Asp Arg Arg Glu

1

5

<210> 20

<211> 9

<212> PRT
<213> Artificial Sequence

<220>
<223> inversed RAD motif peptide

<400> 20

Val Val Cys Asp Ala Arg Arg Arg Cys
1 5

<210> 21
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> inversed RAD motif peptide

<400> 21

Thr His Ser Asp Ala Arg Arg Arg Glu
1 5

<210> 22
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<221> VARIANT
<222> (1, 2, 3, 7, 8, 9)
<223> encoded by randomized DNA sequence: Ala, Cys, Asp, Glu,
Phe, Gly, His, Ile, Lys, Leu, Met, Asn, Pro, Gln, Arg, Ser,
Thr, Val, Trp, Tyr

<400> 22

Xaa Xaa Xaa Arg Ala Asp Xaa Xaa Xaa
1 5

<210> 23
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> RAD motif peptide

<400> 23

Cys Arg Ala Asp Val Pro Leu Cys
1 5

<210> 24
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> RAD motif peptide

<400> 24

Cys Met Ser Arg Ala Asp Arg Pro Cys
1 5

<210> 25
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> CDR consensus part

<400> 25

Val Arg Val Val Cys Arg Ala Asp Lys Arg Cys Tyr Ala Met Asp
1 5 10 15
Val

<210> 26
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> CDR consensus part

<400> 26

Val Arg Val Trp Cys Arg Ala Asp Arg Arg Cys Tyr Ala Met Asp
1 5 10 15
Val

<210> 27
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> CDR consensus part

<400> 27

Val Arg Val Trp Cys Arg Ala Asp Lys Arg Cys Tyr Ala Met Asp
1 5 10 15
Val

<210> 28
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> CDR consensus part

<400> 28

Val Gly Val Val Cys Arg Ala Asp Arg Arg Cys Tyr Ala Met Asp
1 5 10 15
Val

<210> 29
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> CDR consensus part

<400> 29

Val Gly Val Val Cys Arg Ala Asp Lys Arg Cys Tyr Ala Met Asp
1 5 10 15
Val

<210> 30
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> CDR consensus part

<400> 30

Val Gly Val Trp Cys Arg Ala Asp Arg Arg Cys Tyr Ala Met Asp
1 5 10 15
Val

<210> 31
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> CDR consensus part

<400> 31

Val Gly Val Trp Cys Arg Ala Asp Lys Arg Cys Tyr Ala Met Asp

1 5 10 15
Val

<210> 32
<211> 118
<212> PRT
<213> Homo sapiens

<220>
<223> RAD87 part

<400> 32

Glu	Val	Gln	Leu	Leu	Glu	Ser	Gly	Gly	Gly	Leu	Val	Gln	Pro	Gly
1					5				10				15	
Gly	Ser	Leu	Arg	Leu	Ser	Cys	Ala	Gly	Ser	Gly	Phe	Thr	Phe	Ser
					20				25				30	
Ser	Tyr	Ala	Met	His	Trp	Val	Arg	Gln	Ala	Pro	Gly	Lys	Gly	Leu
					35				40				45	
Glu	Trp	Val	Ser	Ala	Ile	Gly	Thr	Gly	Gly	Gly	Thr	Tyr	Tyr	Ala
					50				55				60	
Asp	Ser	Val	Lys	Gly	Arg	Phe	Thr	Ile	Ser	Arg	Asp	Asn	Ala	Lys
					65				70				75	
Asn	Ser	Leu	Tyr	Leu	Gln	Met	Asn	Ser	Leu	Arg	Ala	Glu	Asp	Thr
					80				85				90	
Ala	Val	Tyr	Tyr	Cys	Ala	Arg	Val	Arg	Val	Val	Cys	Arg	Ala	Asp
					95				100				105	
Arg	Arg	Cys	Tyr	Ala	Met	Asp	Val	Trp	Gly	Gln	Gly	Thr		
					110				115					

<210> 33
<211> 118
<212> PRT
<213> Homo sapiens

<220>
<223> RAD9 part

<400> 33

Glu	Val	Gln	Leu	Leu	Glu	Ser	Gly	Gly	Gly	Leu	Val	Gln	Pro	Gly
1					5				10				15	
Gly	Ser	Leu	Arg	Leu	Ser	Cys	Ala	Gly	Ser	Gly	Phe	Thr	Phe	Ser
					20				25				30	
Ser	Tyr	Ala	Met	His	Trp	Val	Arg	Gln	Ala	Pro	Gly	Lys	Gly	Leu
					35				40				45	
Glu	Trp	Val	Ser	Ala	Ile	Gly	Thr	Gly	Gly	Gly	Thr	Tyr	Tyr	Ala
					50				55				60	
Asp	Ser	Val	Lys	Gly	Arg	Phe	Thr	Ile	Ser	Arg	Asp	Asn	Ala	Lys
					65				70				75	
Asn	Ser	Leu	Tyr	Leu	Gln	Met	Asn	Ser	Leu	Arg	Ala	Glu	Asp	Thr
					80				85				90	
Ala	Val	Tyr	Tyr	Cys	Ala	Arg	Val	Arg	Val	Val	Cys	Arg	Ala	Asp
					95				100				105	
Arg	Arg	Cys	Tyr	Ala	Met	Asp	Val	Trp	Gly	Gln	Gly	Thr		
					110				115					

<210> 34
<211> 118
<212> PRT
<213> Homo sapiens

<220>
<223> RAD12 part

<400> 34

Glu	Val	Gln	Leu	Leu	Glu	Ser	Gly	Gly	Gly	Leu	Val	Gln	Pro	Gly
1					5				10				15	
Gly	Ser	Leu	Arg	Leu	Ser	Cys	Ala	Gly	Ser	Gly	Phe	Thr	Phe	Ser
									20			25		30
Ser	Tyr	Ala	Met	His	Trp	Val	Arg	Gln	Ala	Pro	Gly	Lys	Gly	Leu
									35			40		45
Glu	Trp	Val	Ser	Ala	Ile	Gly	Thr	Gly	Gly	Gly	Thr	Tyr	Tyr	Ala
									50			55		60
Asp	Ser	Val	Lys	Gly	Arg	Phe	Thr	Ile	Ser	Arg	Asp	Asn	Ala	Lys
								65			70		75	
Asn	Ser	Leu	Tyr	Leu	Gln	Met	Asn	Ser	Leu	Arg	Ala	Glu	Asp	Thr
								80			85		90	
Ala	Val	Tyr	Tyr	Cys	Ala	Arg	Val	Arg	Val	Val	Cys	Arg	Ala	Asp
								95			100		105	
Arg	Arg	Cys	Tyr	Ala	Met	Asp	Val	Trp	Gly	Gln	Gly	Thr		
								110			115			

<210> 35
<211> 118
<212> PRT
<213> Homo sapiens

<220>
<223> RAD34 part

<400> 35

Glu	Val	Gln	Leu	Leu	Glu	Ser	Gly	Gly	Gly	Leu	Val	Gln	Pro	Gly
1					5				10				15	
Gly	Ser	Leu	Arg	Leu	Ser	Cys	Ala	Gly	Ser	Gly	Phe	Thr	Phe	Ser
									20			25		30
Ser	Tyr	Ala	Met	His	Trp	Val	Arg	Gln	Ala	Pro	Gly	Lys	Gly	Leu
									35			40		45
Glu	Trp	Val	Ser	Ala	Ile	Gly	Thr	Gly	Gly	Gly	Thr	Tyr	Tyr	Ala
								50			55		60	
Asp	Ser	Val	Lys	Gly	Arg	Phe	Thr	Ile	Ser	Arg	Asp	Asn	Ala	Lys
								65			70		75	
Asn	Ser	Leu	Tyr	Leu	Gln	Met	Asn	Ser	Leu	Arg	Ala	Glu	Asp	Thr
								80			85		90	
Ala	Val	Tyr	Tyr	Cys	Ala	Arg	Val	Arg	Val	Val	Cys	Arg	Ala	Asp
								95			100		105	
Arg	Arg	Cys	Tyr	Ala	Met	Asp	Val	Trp	Gly	Gln	Gly	Thr		
								110			115			

<210> 36
<211> 118
<212> PRT
<213> *Homo sapiens*

<220>
<223> RAD3 part

<400> 36

Glu	Val	Gln	Leu	Leu	Glu	Ser	Gly	Gly	Gly	Leu	Val	Gln	Pro	Gly
1					5				10					15
Gly	Ser	Leu	Arg	Leu	Ser	Cys	Ala	Gly	Ser	Gly	Phe	Thr	Phe	Ser
						20				25				30
Ser	Tyr	Ala	Met	His	Trp	Val	Arg	Gln	Ala	Pro	Gly	Lys	Gly	Leu
							35			40				45
Glu	Trp	Val	Ser	Ala	Ile	Gly	Thr	Gly	Gly	Gly	Thr	Tyr	Tyr	Ala
						50				55				60
Asp	Ser	Val	Lys	Gly	Arg	Phe	Thr	Ile	Ser	Arg	Asp	Asn	Ala	Lys
						65				70				75
Asn	Ser	Leu	Tyr	Leu	Gln	Met	Asn	Ser	Leu	Arg	Ala	Glu	Asp	Thr
						80				85				90
Ala	Val	Tyr	Tyr	Cys	Ala	Arg	Val	Arg	Val	Val	Cys	Arg	Ala	Asp
						95				100				105
Arg	Arg	Cys	Tyr	Ala	Met	Asp	Val	Trp	Gly	Gln	Gly	Thr		
						110				115				

<210> 37
<211> 118
<212> PRT
<213> *Homo sapiens*

<220>
<223> RAD32 part

<400> 37

Glu	Val	Gln	Leu	Leu	Glu	Ser	Gly	Gly	Gly	Leu	Val	His	Pro	Gly
1					5					10				15
Gly	Ser	Leu	Arg	Leu	Ser	Cys	Ala	Gly	Ser	Gly	Phe	Thr	Phe	Ser
									20			25		30
Ser	Tyr	Ala	Met	His	Trp	Val	Arg	Gln	Ala	Pro	Gly	Lys	Gly	Leu
									35			40		45
Glu	Trp	Val	Ser	Ala	Ile	Gly	Thr	Gly	Gly	Gly	Thr	Tyr	Tyr	Ala
									50			55		60
Asp	Ser	Val	Lys	Gly	Arg	Phe	Thr	Val	Ser	Arg	Asp	Asn	Ser	Gln
									65			70		75
Ser	Thr	Ala	Tyr	Leu	Gln	Ile	Asn	Ser	Leu	Arg	Ala	Glu	Asp	Thr
									80			85		90
Ala	Val	Tyr	Tyr	Cys	Ala	Arg	Val	Gly	Val	Trp	Cys	Arg	Ala	Asp
									95			100		105
Lys	Arg	Cys	Tyr	Ala	Met	Asp	Val	Trp	Gly	Gln	Gly	Thr		
									110			115		

<210> 38
<211> 118
<212> PRT
<213> Homo sapiens

<220>
<223> RAD88 part

<400> 38

Glu	Val	Gln	Leu	Leu	Glu	Ser	Gly	Gly	Gly	Leu	Val	His	Pro	Gly
1					5				10			15		
Gly	Ser	Leu	Arg	Leu	Ser	Cys	Ala	Gly	Ser	Gly	Phe	Thr	Phe	Ser
						20			25			30		
Ser	Tyr	Ala	Met	His	Trp	Val	Arg	Gln	Ala	Pro	Gly	Lys	Gly	Leu
						35			40			45		
Glu	Trp	Val	Ser	Ala	Ile	Gly	Thr	Gly	Gly	Thr	Tyr	Tyr	Tyr	Ala
						50			55			60		
Asp	Ser	Val	Lys	Gly	Arg	Phe	Thr	Val	Ser	Arg	Asp	Asn	Ser	Gln
						65			70			75		
Ser	Thr	Ala	Tyr	Leu	Gln	Ile	Asn	Ser	Leu	Arg	Ala	Glu	Asp	Thr
						80			85			90		
Ala	Val	Tyr	Tyr	Cys	Ala	Arg	Val	Gly	Val	Trp	Cys	Arg	Ala	Asp
						95			100			105		
Lys	Arg	Cys	Tyr	Ala	Met	Asp	Val	Trp	Gly	Gln	Gly	Thr		
						110			115					

<210> 39
<211> 119
<212> PRT
<213> Homo sapiens

<220>
<223> RAD1 part

<400> 39

Glu	Val	Gln	Leu	Leu	Glu	Ser	Gly	Gly	Gly	Leu	Val	Gln	Pro	Gly
1					5				10			15		
Gly	Ser	Leu	Arg	Leu	Ser	Cys	Ala	Ala	Ser	Gly	Phe	Thr	Phe	Ser
						20			25			30		
Phe	Tyr	Gly	Met	Ser	Trp	Val	Arg	Gln	Ala	Pro	Gly	Lys	Gly	Leu
						35			40			45		
Glu	Trp	Val	Ser	Gly	Val	Ser	Ser	Gly	Ile	Thr	Thr	Tyr	Tyr	
						50			55			60		
Ala	Ala	Ser	Val	Arg	Gly	Arg	Phe	Thr	Ile	Ser	Arg	Asp	Asn	Ser
						65			70			75		
Lys	Asn	Thr	Leu	Tyr	Leu	Gln	Met	Asn	Ser	Leu	Arg	Ala	Glu	Asp
						80			85			90		
Thr	Ala	Val	Tyr	Tyr	Cys	Ala	Arg	Val	Arg	Thr	His	Ser	Arg	Ala
						95			100			105		
Asp	Arg	Arg	Glu	Tyr	Ala	Met	Asp	Val	Trp	Gly	Gln	Gly	Thr	
						110			115					

<210> 40

<211> 3
<212> PRT
<213> Homo sapiens

<220>
<223> RGD motif

<400> 40

Arg Gly Asp
1

<210> 41
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> RAD motif

<400> 41

Arg Ala Asp
1

<210> 42
<211> 3
<212> PRT
<213> Mus musculus

<220>
<223> RYD motif

<400> 42

Arg Tyr Asp
1

<210> 43
<211> 9
<212> PRT
<213> Homo sapiens

<220>
<223> RAD1 part

<400> 43

Thr His Ser Arg Ala Asp Arg Arg Glu
1 5

<210> 44
<211> 9

<212> PRT
<213> Homo sapiens

<220>
<223> RAD3 part

<400> 44

Val Val Cys Arg Ala Asp Arg Arg Cys
1 5

<210> 45
<211> 9
<212> PRT
<213> Homo sapiens

<220>
<223> RAD4 part

<400> 45

Val Trp Cys Arg Ala Asp Arg Arg Cys
1 5

<210> 46
<211> 9
<212> PRT
<213> Homo sapiens

<220>
<223> RAD9 part

<400> 46

Val Val Cys Arg Ala Asp Arg Arg Cys
1 5

<210> 47
<211> 9
<212> PRT
<213> Homo sapiens

<220>
<223> RAD11 part

<400> 47

Val Trp Cys Arg Ala Asp Arg Arg Cys
1 5

<210> 48
<211> 9
<212> PRT

<213> Homo sapiens

<220>

<223> RAD12 part

<400> 48

Val Val Cys Arg Ala Asp Arg Arg Cys

1 5

<210> 49

<211> 9

<212> PRT

<213> Homo sapiens

<220>

<223> RAD32 part

<400> 49

Val Trp Cys Arg Ala Asp Lys Arg Cys

1 5

<210> 50

<211> 9

<212> PRT

<213> Homo sapiens

<220>

<223> RAD34 part

<400> 50

Val Val Cys Arg Ala Asp Arg Arg Cys

1 5

<210> 51

<211> 9

<212> PRT

<213> Homo sapiens

<220>

<223> RAD87 part

<400> 51

Val Val Cys Arg Ala Asp Arg Arg Cys

1 5

<210> 52

<211> 9

<212> PRT

<213> Homo sapiens

<220>
<223> RAD88 part

<400> 52

Val Trp Cys Arg Ala Asp Lys Arg Cys
1 5

<210> 53
<211> 18
<212> PRT
<213> Homo sapiens

<220>
<223> Anti-gp120 Fab part

<400> 53

Val Gly Pro Tyr Ser Trp Asp Asp Ser Pro Asp Gln Asn Tyr Tyr
1 5 10 15
Met Asp Val

<210> 54
<211> 18
<212> PRT
<213> Homo sapiens

<220>
<221> VARIANT
<222> (4,5,6,10,11,12)
<223> Fab library part; Ala, Cys, Asp, Glu, Phe, Gly, His, Ile,
Lys, Leu, Met, Asn, Pro, Gln, Arg, Ser, Thr, Val, Trp, Tyr

<400> 54

Val Gly Cys Xaa Xaa Xaa Arg Gly Asp Xaa Xaa Xaa Cys Tyr Tyr
1 5 10 15
Met Asp Val

<210> 55
<211> 18
<212> PRT
<213> Homo sapiens

<220>
<223> Fab-4 part

<400> 55

Val Gly Cys Thr Gly Gln Arg Gly Asp Trp Arg Ser Cys Tyr Tyr
1 5 10 15
Met Asp Val

<210> 56
<211> 18
<212> PRT
<213> Homo sapiens

<220>
<223> Fab-7 part

<400> 56

Val Gly Cys Thr Tyr Gly Arg Gly Asp Thr Arg Asn Cys Tyr Tyr
1 5 10 15
Met Asp Val

<210> 57
<211> 18
<212> PRT
<213> Homo sapiens

<220>
<223> Fab-8 part

<